A Reaction Center-dependent Photoprotection Mechanism in a Highly Robust Photosystem II from an Extremophilic Red Alga, Cyanidioschyzon merolae

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Published in:
J. Biol. Chem.

DOI:
10.1074/jbc.M113.484659

SUPPLEMENTAL DATA

Table S1. LC-MS/MS analysis of the *C. merolae* PSII subunits. Molecular mass for each protein is calculated following translation of the corresponding cDNA sequence.

Accession[a]	Protein identified	M_{wt} (Da)[b]	PLGS Score[c]	Peptides	Coverage (%)
CMV208C	PsbV (cyt c_{550})	16596	169103.4	27	65.3
CMI290C	PsbO (33 kDa protein)	35428	105083.5	72	62.0
CMC133C	PsbQ′	23599	43222.95	40	50.2
CMV082C	PsbC (CP43)	50259	29911.51	25	30.3
CMI248C	PsbU (12 kDa protein)	16827	25700.32	23	46.1
CMV124C	PsbB (CP47)	56248	23602.2	48	43.6
CMV127C	PsbH	7219	22342.63	3	21.9
CMV047C	PsbA (D1)	39477	14840.17	13	25.6
CMV081C	PsbD (D2)	39264	14821.83	12	23.9
CMV231C	PsbE (α-cyt b_{559})	9203	6165.97	8	46.9
CMK176C	Psb27	21981	2056.627	12	42.9
CMT182C	PsbM	16113	1657.718	3	24.0
CMV089C	PsbW	12572	721.237	2	16.5
CMV140C	PsbK	4892	1150.222	2	46.5
CMV230C	PsbF (β-cyt b_{559})	4697	607.9701	2	30
CMV229C	PsbL	4378	346.6986	6	18.4
CMV240C	PsbI	4471	209.368	9	36.8

[a] accession numbers and most of the descriptions are taken from (86).
[b] molecular mass for each protein is calculated following translation of the corresponding cDNA sequence.
[c] PLGS Score is calculated by the Protein Lynx Global Server (PLGS 2.4) software to analyse all available mass spectrometry data and is a statistical measure of accuracy of identification. A higher score implies greater confidence of protein identity.